AMENDMENTS TO THE SPECIFICATION:

Please amend the specification as follows:

Paragraph at page 1, lines 3-4 (cross-reference to related applications):

This application is a divisional of U.S. Application No. 09/665,308, filed September 19, 2000, now pending and herein incorporated by reference, which is a continuation of International Application No. PCT/US99/06047, filed March 19, 1999, now expired, which claims the benefit of U.S. Provisional Application No. 60/078,948, filed March 23, 1998, now expired.

Paragraph at page 3, lines 19-20:

Figures 2A and 2B show ~~Figure 2 shows~~ a comparison of the amino acid sequences set forth in SEQ ID NOs:8, 10, 12 and 14 and the *A. thaliana* cyclin delta-1 sequence, SEQ ID NO:30.

Paragraph at page 3, lines 21-22:

Figures 3A and 3B show ~~Figure 3 shows~~ a comparison of the amino acid sequences set forth in SEQ ID NOs:18 and 22 and the *Nicotiana* ~~*Nicotina*~~ *tabacum* sequence, SEQ ID NO:31.

Paragraph at page 7, lines 5-27:

A "substantial portion" of an amino acid or nucleotide sequence comprises enough of the amino acid sequence of a polypeptide or the nucleotide sequence of a gene to afford putative identification of that polypeptide or gene, either by manual evaluation of the sequence by one skilled in the art, or by computer-automated sequence comparison and identification using algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1993) *J. Mol. Biol. 215*:403-410; ~~see also www.ncbi.nlm.nih.gov/BLAST/~~). In general, a sequence of ten or more contiguous amino acids or thirty or more nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene specific oligonucleotide probes comprising 20-30 contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12-15 bases may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises enough of the sequence to afford specific identification and/or isolation of

a nucleic acid fragment comprising the sequence. The instant specification teaches partial or complete amino acid and nucleotide sequences encoding one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

Paragraph at page 18, lines 8-25:

ESTs encoding cyclin proteins were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1993) *J. Mol. Biol. 215*:403-410; ~~see also www.ncbi.nlm.nih.gov/BLAST/~~) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish, W. and States, D. J. (1993) *Nature Genetics 3*:266-272 and Altschul, Stephen F., et al. (1997) *Nucleic Acids Res. 25*:3389-3402) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.

Table 5 on page 21:

TABLE 5

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide Sequences of cDNA Clones Encoding Polypeptides Homologous to *Arabidopsis thaliana* Cyclin Delta-1 Proteins

Clone	SEQ ID NO.	Percent Similarity
Contig Composed of: p0098.cdfae90r p0116.cesaf50r p0128.cpiad46rb	8	31% ~~29%~~
rl0n.pk0031.e6	10	32% ~~31%~~
Contig Composed of: sah1c.pk003.i7 sr1.pk0001.g5	12	57% ~~54%~~
se6.pk0028.f11	14	57% ~~54%~~

Table 7 on page 23:

TABLE 7

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide Sequences of cDNA Clones Encoding Polypeptides Homologous to ~~*Nicotina*~~ *Nicotiana tabacum* Cyclin Delta-2 Proteins

Clone	SEQ ID NO.	Percent Similarity
ceb5.pk0049.h5	18	38.4% ~~37%~~
wre1n.pk0104.c1	22	32.5%